RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/810, 063B_
Source: _1FW16_
Date Processed by STIC: _5/5/06_

ENTERED

IFW16

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      RAW SEQUENCE LISTING              DATE: 05/05/2006
      PATENT APPLICATION:  US/10/810,063B     TIME: 10:10:07

      Input Set : 3:\INGN106.APP.txt
      Output Set: N:\CRF4\05052006\J810063B.raw
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 3 <110> APPLICANT: WOLD, WILLIAM
 4       TOLLEFSON, ANN
 6 <120> TITLE OF INVENTION: ADENOVIRUS REPLICATION-COMPETENT VECTORS EXPRESSING
 7       TRAIL
 9 <130> FILE REFERENCE: INGN:106US
11 <140> CURRENT APPLICATION NUMBER: 10/810,063B
12 <141> CURRENT FILING DATE: 2004-03-26
14 <150> PRIOR APPLICATION NUMBER: 60/458,493
15 <151> PRIOR FILING DATE: 2003-03-28
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1769
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (88)..(933)
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33 ttacagcagt cagactctga caggatc atg gct atg atg gag gtc cag ggg gga 114
34                                 Met Ala Met Met Glu Val Gln Gly Gly
35                                   1               5
37 ccc agc ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg ctc    162
38 Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu
39  10              15                  20                  25
41 ctg cag tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac gag    210
42 Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu
43              30                  35                  40
45 ctg aag cag atg cag gac aag tac tcc aaa agt ggc att gct tgt ttc    258
46 Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe
47          45                  50                  55
49 tta aaa gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt atg    306
50 Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met
51      60                  65                  70
53 aac agc ccc tgc tgg caa gtc aag tgg caa ctc cgt cag ctc gtt aga    354
54 Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg
55      75                  80                  85
57 aag atg att ttg aga acc tct gag gaa acc att tct aca gtt caa gaa    402
58 Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
59  90                  95                  100                 105
61 aag caa caa aat att tct ccc cta gtg aga gaa aga ggt cct cag aga    450
62 Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
```

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 63               110            115            120
 65 gta gca gct cac ata act ggg acc aga gga aga agc aac aca ttg tct   498
 66 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
 67          125            130            135
 69 tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc   546
 70 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
 71          140            145            150
 73 tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac ttg   594
 74 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
 75     155            160            165
 77 agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc tat   642
 78 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
 79 170            175            180            185
 81 tcc caa aca tac ttt cga ttt cag gag gaa ata aaa gaa aac aca aag   690
 82 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
 83          190            195            200
 85 aac gac aaa caa atg gtc caa tat att tac aaa tac aca agt tat cct   738
 86 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
 87          205            210            215
 89 gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct aaa   786
 90 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
 91          220            225            230
 93 gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag   834
 94 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
 95     235            240            245
 97 ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg   882
 98 Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
 99 250            255            260            265
101 ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc   930
102 Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
103               270            275            280
105 taa ctgacctgga aagaaaaagc aataacctca aagtgactat tcagttttca        983
108 ggatgataca ctatgaagat gtttcaaaaa atctgaccaa aacaaacaaa cagaaaacag 1043
110 aaaacaaaaa aacctctatg caatctgagt agagcagcca caaccaaaaa attctacaac 1103
112 acacactgtt ctgaaagtga ctcacttatc ccaagaaaat gaaattgctg aaagatcttt 1163
114 caggactcta cctcatatca gtttgctagc agaaatctag aagactgtca gcttccaaac 1223
116 attaatgcaa tggttaacat cttctgtctt tataatctac tccttgtaaa gactgtagaa 1283
118 gaaagcgcaa caatccatct ctcaagtagt gtatcacagt agtagcctcc aggtttcctt 1343
120 aagggacaac atccttaagt caaaagagag aagaggcacc actaaaagat cgcagtttgc 1403
122 ctggtgcagt ggctcacacc tgtaatccca acattttggg aacccaaggt gggtagatca 1463
124 cgagatcaag agatcaagac catagtgacc aacatagtga aaccccatct ctactgaaag 1523
126 tgcaaaaatt agctgggtgt gttggcacat gcctgtagtc ccagctactt gagaggctga 1583
128 ggcaggagaa tcgtttgaac ccgggaggca gaggttgcag tgtggtgaga tcatgccact 1643
130 acactccagc ctggcgacag agcgagactt ggtttcaaaa aaaaaaaaa aaaaaaactt 1703
132 cagtaagtac gtgttatttt tttcaataaa attctattac agtatgtcaa aaaaaaaaaa 1763
134 aaaaaa                                                            1769
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 281
139 <212> TYPE: PRT
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143 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
144  1               5                  10                  15
145 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
146             20                  25                  30
147 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
148          35                  40                  45
149 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
150      50                  55                  60
151 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
152  65                  70                  75                  80
153 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
154              85                  90                  95
155 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
156             100                 105                 110
157 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
158             115                 120                 125
159 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
160         130                 135                 140
161 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
162 145                 150                 155                 160
163 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
164             165                 170                 175
165 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
166             180                 185                 190
167 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
168         195                 200                 205
169 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
170     210                 215                 220
171 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
172 225                 230                 235                 240
173 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
174             245                 250                 255
175 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
176             260                 265                 270
177 Ser Phe Phe Gly Ala Phe Leu Val Gly
178         275                 280
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 14
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <221> NAME/KEY: modified_base /
189 <222> LOCATION: (3)..(12)
190 <223> OTHER INFORMATION: n = a, c, g and/or t/u
192 <220> FEATURE:
193 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
194         Primer
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RAW SEQUENCE LISTING   DATE: 05/05/2006
PATENT APPLICATION: **US/10/810,063B**   TIME: 10:10:07

Input Set : **E:\INGN106.APP.txt**
Output Set: **N:\CRF4\05052006\J810063B.raw**

196 <400> SEQUENCE: 3
W--> 197 **ctngaanntt cnag**   **14**

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/05/2006
PATENT APPLICATION: **US/10/810,063B**   TIME: 10:10:08

Input Set : **E:\INGN106.APP.txt**
Output Set: **N:\CRF4\05052006\J810063B.raw**

<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; N Pos. 3,7,8,12

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/810,063B

DATE: 05/05/2006
TIME: 10:10:08

Input Set : **E:\INGN106.APP.txt**
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L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0